1: Ann Hum Genet. 1999 Jul;63 (Pt 4):277-84. Related Articles, L

Allelic diversity of the human plasma alpha(1,3)fucosyltransferase gene (FUT6).

Pang H, Koda Y, Soejima M, Schlaphoff T, du Toit ED, Kimura H.

Department of Forensic Medicine, Kurume University School of Medicine, Fukuoka, Japan.

The 1080-bp coding region of the human plasma alpha(1,3)fucosyltransferase gene (FUT was sequenced in a total of 161 individuals (322 chromosomes) drawn from three populations, involving 56 Africans (Xhosa), 52 European-Africans of South Africa, and Japanese. In addition to six reported base substitutions, eleven new base substitutions an single base insertion were found in the coding region of the FUT6. Eleven functional and four null alleles were encountered, of which 10 alleles were novel alleles identified in th study. Two null alleles have been identified previously, whereas two novel null alleles, which contained a single base (cytosine) insertion at nucleotide 499, were found in a Xh population. The allelic distributions of FUT6 were different among these three populatio The heterozygosity of FUT6 was 0.860, 0.699, and 0.632, in Xhosa, European-African (South Africa), and in Japanese populations, respectively. The extensive DNA sequence diversity of the FUT6 may be suitable for application as a tool in genetic studies for modern human evolution.

PMID: 10738539 [PubMed - indexed for MEDLINE]

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Related Articles, L

The alpha1-6-fucosyltransferase gene and its biological significance.

Miyoshi E, Noda K, Yamaguchi Y, Inoue S, Ikeda Y, Wang W, Ko JH, Uozumi N, L W, Taniguchi N.

Department of Biochemistry, Osaka University Medical School, Room B-1, 2-2 Yamadaoka, Suita, Osaka, Japan.

GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alpha1-6-fucosyltransferase (alpha1-6FucT catalyzes the transfer of fucose from GDP-Fuc to N-linked type complex glycoproteins. This enzyme was purified from a human fibroblast cell line, porcine brain, a human gast cancer cell line and human blood platelets. cDNA cloning of porcine and human alpha1-6FucT was performed from a porcine brain and gastric cancer cell cDNA libraries, respectively. Their homology is 92.2% at the nucleotide level and 95.7% at the amino ac level. No putative N-glycosylation sites were found in the predicted amino acid sequence No homology to other fucosyltransferases such as alpha1-2FucT, alpha1-3FucT and alpha1-4FucT was found except for a region consisting of nine amino acids. The alpha1-6FucT gene is located at chromosome 14q24.3, which is also a different location from other fucosyltransferases reported to date. The alpha1-6FucT gene is the oldest gene fam in the phylogenic trees among the nine cloned fucosyltransferase genes. alpha1-6FucT is widely expressed in various rat tissues and the expression of alpha1-6FucT in the liver is enhanced during hepatocarcinogenesis of LEC rats which develop hereditary hepatitis an hepatomas. In cases of human liver diseases, alpha1-6FucT is expressed in both hepatom tissues and their surrounding tissues with chronic liver disease, but not in the case of normal liver. Serum alpha1-6-fucosylated alpha-fetoprotein (AFP) has been employed fo an early diagnosis of patients with hepatoma. The mechanisms by which alpha1-6 fucosylation of AFP occurs in the hepatoma is not due to the up-regulation of alpha1-6FucT alone. Interestingly, when the alpha1-6FucT gene is transfected into Hep3B, a human hepatoma cell line, tumor formation in the liver of nude mice after splenic injecti is dramatically suppressed. In this review, we focus on alpha1-6FucT and summarize its properties, gene expression and biological significance.

Publication Types:

- Review
- Review, Tutorial

PMID: 10580126 [PubMed - indexed for MEDLINE]

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1: J Immunol. 1999 Oct 1;163(7):3746-52. Related Articles, L

Alpha(1,3)-fucosyltransferase VII and alpha(2,3)-sialyltransferase IV are up-regulated in activated CD4 T cells and maintained after their differentiation into Th1 and migration into inflammatory sites.

Blander JM, Visintin I, Janeway CA Jr, Medzhitov R.

Section of Immunobiology, Yale University School of Medicine, Howard Hughes Medic Institute, New Haven, CT 06520, USA.

Activated Th1 CD4 T cells bind to P-selectin and migrate into inflamed tissue, whereas Th2 cells do not. We show that alpha(1, 3)-fucosyltransferase VII (FucT-VII) and alpha(3)-sialyltransferase IV (ST3GalIV), which are crucial for the biosynthesis of functional P selectin ligands, are absent in naive CD4 T cells, but are rapidly up-regulated upon activation. Th1 or Th2 differentiation in the presence of polarizing cytokines leads to down-regulation of FucT-VII mRNA selectively in Th2 but not in Th1 cells. Influencing the differentiation by varying the priming dose of antigenic peptide results in similar Fuc VII down-regulation only in Ag-specific Th2 cells. ST3GalIV levels remain elevated. FucT-VII and ST3GalIV mRNAs are also up-regulated by Th1 cells primed in vivo and recruited into the lymph nodes draining delayed-type hypersensitivity sites. We identify FucT-VII gene expression as a principal difference between Th1 and Th2 cells, and underscore the importance of FucT-VII and ST3GalIV expression for the biosynthesis of functional selectin ligands.

PMID: 10490970 [PubMed - indexed for MEDLINE]

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J Biol Chem. 1999 Jul 30;274(31):21830-9.
PMID: 10419500 [PubMed - indexed for MEDLINE]

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Reconstitution of functional L-selectin ligands on a cultured human endothelial cell line by cotransfection of alpha1-->3 fucosyltransferase VII and newly cloned GlcNAcbeta:6 sulfotransferase cDNA.
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6: Gorelik E, Xu F, Henion T, Anaraki F, Galili U. Related Articles, Li

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Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase capable of synthesizing the sialyl Lewis x determinant.
J Biol Chem. 1994 Aug 12;269(32):20806. No abstract available.
PMID: 8051184 [PubMed - indexed for MEDLINE]

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Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase capable of synthesizing the sialyl Lewis x determinant.
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Eur J Biochem. 1983 Feb 1;130(2):347-51.
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1: J Biol Chem. 1994 Aug 12;269(32):20806. Related Articles, L

Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3 fucosyltransferase capable of synthesizing the sialyl Lewis x determinant.

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Purification, cDNA cloning, and expression of GDP-L-Fuc:Asn-linked GlcNAc alpha1,3-fucosyltransferase from mung beans.

Leiter H, Mucha J, Staudacher E, Grimm R, Glossl J, Altmann F.

Institute of Chemistry, Universitat fur Bodenkultur, Muthgasse 18, 1190 Wien, Austria. faltmann@edv2.boku.ac.at

Substitution of the asparagine-linked GlcNAc by alpha1,3-linked fucose is a widespread feature of plant as well as of insect glycoproteins, which renders the N-glycan immunogenic. We have purified from mung bean seedlings the GDP-L-Fuc:Asn-linked GlcNAc alpha1,3-fucosyltransferase (core alpha1,3-fucosyltransferase) that is responsib for the synthesis of this linkage. The major isoform had an apparent mass of 54 kDa and isoelectric points ranging from 6. 8 to 8.2. From that protein, four tryptic peptides were isolated and sequenced. Based on an approach involving reverse transcriptase-polymeras chain reaction with degenerate primers and rapid amplification of cDNA ends, core alpha1,3-fucosyltransferase cDNA was cloned from mung bean mRNA. The 2200-base pair cDNA contained an open reading frame of 1530 base pairs that encoded a 510-amin acid protein with a predicted molecular mass of 56.8 kDa. Analysis of cDNA derived fro genomic DNA revealed the presence of three introns within the open reading frame. Remarkably, from the four exons, only exon II exhibited significant homology to animal and bacterial alpha1,3/4-fucosyltransferases which, though, are responsible for the biosynthesis of Lewis determinants. The recombinant fucosyltransferase was expressed i Sf21 insect cells using a baculovirus vector. The enzyme acted on glycopeptides having glycan structures GlcNAcbeta1-2Manalpha1-3(GlcNAcbeta1-2Manalpha1- 6)Manbeta1 4GlcNAcbet a1-4GlcNAcbeta1-Asn, GlcNAcbeta1-2Manalpha1-3(GlcNAcbeta1- 2Manalpha1- 6)Manbeta1-4GlcNAcbet a1-4(Fucalpha1-6)GlcNAcbeta1-Asn, and GlcNAcbeta1-2Manalpha1-3[Manalpha1-3(Manalpha1-6)Manalpha1-6]Manbeta1 - 4GlcNAcbeta1-4GlcNAcbeta1-Asn but not on, e.g. N-acetyllactosamine. The structure o the core alpha1,3-fucosylated product was verified by high performance liquid chromatography of the pyridylaminated glycan and by its insensitivity to N-glycosidase as revealed by matrix-assisted laser desorption/ionization time of flight mass spectromet

PMID: 10419500 [PubMed - indexed for MEDLINE]

1: J Biochem (Tokyo). 1997 Mar;121(3):626-32. Related Articles, L

Purification and cDNA cloning of GDP-L-Fuc:N-acetyl-beta-D-glucosaminide:alpha1-6 fucosyltransferase (alpha1-6 FucT) from human gastric cancer MKN45 cells.

Yanagidani S, Uozumi N, Ihara Y, Miyoshi E, Yamaguchi N, Taniguchi N.

Department of Biochemistry, Osaka University Medical School, Suita.

GDP-L-Fuc:N-acetyl-beta-D-glucosaminide:alpha1-6 fucosyltransferase (alpha1-6 FucT which catalyzes the transfer of fucose from GDP-Fuc to N-linked type complex glycopeptides, was purified from a culture supernatant of human gastric cancer cell line MKN45. The purification procedures included chromatographies on Q-Sepharose Fast Flow, synthetic GDP-hexanolamine-Sepharose, and GnGn-bi-Asn-Sepharose columns. SDS-PAGE of the purified enzyme gave a major band corresponding to an apparent molecular mass of 60 kDa. The enzyme was recovered in a 12% final yield with an approximately 4,600-fold increase in specific activity. The pH optimum was 7.5, and the enzyme was fully active in the presence of 5 mM EDTA and did not require divalent cations, Mg2+ and Ca2+. Oligonucleotide primers designed from partial amino acid sequences were used to amplify and clone alpha1-6 FucT cDNA from a cDNA library of MKN45 cells. The cDNA encodes 575 amino acids in length, and contains the predicted terminal and internal amino acid sequences derived on lysyl endopeptidase digestion. Th homology to porcine brain alpha1-6 FucT is 92.2% at the nucleotide level and 95.7% at amino acid level. No putative N-glycosylation sites were found in the predicted amino ac sequence of the human MKN45 cell enzyme or that of porcine brain. Thus, the enzyme i distinct from other fucosyltransferases which catalyze alpha1-2, alpha1-3, and alpha1-4 fucose addition.

PMID: 9133635 [PubMed - indexed for MEDLINE]

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Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can for the H blood group antigen.

Larsen RD, Ernst LK, Nair RP, Lowe JB.

Howard Hughes Medical Institute, Ann Arbor, MI.

We have previously used a gene-transfer scheme to isolate a human genomic DNA fragment that determines expression of a GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase [alpha(1,2)FT; EC 2.4.1.69]. Although this fragment determined expression of an alpha(1,2)FT whose kinetic properties mirror those of the human H blo group alpha(1,2)FT, their precise nature remained undefined. We describe here the molecular cloning, sequence, and expression of a human cDNA corresponding to these human genomic sequences. When expressed in COS-1 cells, this cDNA directs expressio of cell surface H structures and a cognate alpha(1,2)FT activity with properties analogou to the human H blood group alpha(1,2)FT. The cDNA sequence predicts a 365-amino ac polypeptide characteristic of a type II transmembrane glycoprotein with a domain structu analogous to that of other glycosyltransferases but without significant primary sequence similarity to these or other known proteins. To directly demonstrate that the cDNA enco an alpha(1,2)FT, the COOH-terminal domain predicted to be Golgi-resident was express in COS-1 cells as a catalytically active, secreted, and soluble protein A fusion peptide. Southern blot analysis showed that this cDNA identifies DNA sequences syntenic to the human H locus on chromosome 19. These results strongly suggest that this cloned alpha (1,2)FT cDNA represents the product of the human H blood group locus.

PMID: 2118655 [PubMed - indexed for MEDLINE]

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